miR-1343-3p inhibits autophagy by directly targeting ATG7 in multiple myeloma cells

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Abstract. Multiple myeloma (MM) is the second most common type of hematological malignancy globally. Despite application of several new drugs, such as daratumumab, bortezomib/lenalidomide/dexamethasone, in combination with hematopoietic stem cell transplantation, overall prognosis remains poor and the pathological mechanism of MM is still unknown. The present study used TargetScan to predict autophagy-related 7 (ATG7) as a candidate target gene of microRNA (miR)-1343-3p and confirmed the interaction between miR-1343-3p and the ATG7 3' untranslated region (3'UTR) using a dual-luciferase reporter assay. In U266 and RPMI-8226 MM cell lines, miR-1343-3p mimic transfection decreased mRNA and protein levels of ATG7, while miR-1343-3p inhibition increased ATG7 expression levels using reverse transcription-qPCR and western blot analysis. miR-1343-3p mimic transfection inhibited U266 and RPMI-8226 cell survival. Finally, miR-1343-3p regulated ATG7 and autophagy in MM cells using western blot analysis. The present findings suggested that miR-1343-3p may regulate ATG7 and autophagy by directly targeting the 3'UTR of ATG7. To the best of our knowledge, there are no direct data showing the roles of miR-1343-3p in development of MM; however, miR-1343-3p may be considered a potential target for MM treatment.

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Introduction

Multiple myeloma (MM) is the second most common type of hematological malignancy, accounting for ~1% of all malignancies and ~13% of hematological tumors in 2019 (1). MM is a malignant disease mediated by B lymphocytes and characterized by malignant proliferation of bone marrow monoclonal plasma cells with extensive infiltration leading to normal bone marrow blockage (2). With a median survival time of 5-7 years after diagnosis, there is currently no cure for MM except allogeneic hematopoietic stem cell transplantation. With a median survival of 5-7 years after diagnosis, MM is currently regarded as an incurable disease (3).

MicroRNAs (miRNAs/miRs) are small non-coding RNAs that regulate expression of target genes by binding to them. Notably, they regulate oncogenes or oncogene-like proteins, thus serving a key role in biological processes such as cell proliferation, autophagy, apoptosis and differentiation (4). Numerous studies have shown that specific miRNAs are expressed at abnormally high levels in MM cell lines and patient samples, exhibiting potential as therapeutic targets (5,6). miR-1343-3p is downregulated in cancer tissue, including pancreatic, prostate and colon cancer (7). However, the role of miR-1343-3p in the progression of MM remains unclear.

The reports have indicated that salidroside, a bioactive phenolic glycoside compound isolated from various plant species belonging to the family Crassulaceae can inhibit proliferation and invasion of gastric cancer cells by upregulating miR-1343-3p, which downregulates MAP3K6/MMP24 signaling molecules (8). Conversely, fat mass and obesity-associated protein)-mediated inhibition of miR-1343-3p induces docetaxel resistance in breast cancer cells (9). Similarly, circular RNAs targeting and inhibiting miR-1343-3p enhance TGFβ/Smad3/epithelial-mesenchymal transition (EMT) signaling, resulting in deterioration of non-small cell lung cancer (NSCLC) and ovarian cancer (10). Long non-coding (lnc)RNA LINC02323, by targeting and

inhibiting miR-1343-3p, has been reported to upregulate EMT-associated genes, promoting the metastasis of lung adenocarcinoma cells (5). Other lncRNAs) regulate the MAPK and PARP1/PTEN/AKT pathways by binding and sequestering miR-1343-3p, thereby promoting progression of pancreatic (7) and colorectal cancer (11), respectively. Additionally, certain lncRNAs, by sequestering miR-1343-3p, may decrease its inhibitory effect on genes such as recombinant Annexin A11 and NFIX (Nuclear Factor I X) (12), thereby promoting the proliferation, invasion and survival of glioma cells (13) and NSCLC.

lncRNA GAS8-AS1 (GAS8 antisense RNA 1) inhibits autophagy in papillary thyroid cancer cells by regulating the miR-1343-3p/autophagy-related 7 (ATG7) pathway to promote cancer cell proliferation (14). miR-1343-3p can bind to the 3' untranslated region (UTR) of ATG7 mRNA, leading to its degradation or translational suppression, thereby reducing ATG7 protein levels. When miR-1343-3p binds to GAS8-AS1, its binding to ATG7 is weakened, thus decreasing its inhibitory effect on ATG7 (14,15) and enhancing the autophagy process and promoting cancer cell survival. ATG7 is a protein-coding gene that primarily encodes an E1-like activating enzyme required for autophagy and cytoplasmic-to-vesicular transport; ATG7 has also been observed to be upregulated in malignant tumors, including lung, ovarian and thyroid cancer (16). Its encoded protein regulates tumor suppressor p53-dependent cell cycle and apoptotic pathways during prolonged metabolic stress and deletion of ATG7 may lead to increased DNA damage and p53-dependent apoptosis (17).

MM cells produce large amounts of monoclonal immunoglobulins, resulting in endoplasmic reticulum stress, and autophagy can degrade excess protein aggregates to protect MM cells (18). Autophagy plays an irreplaceable role in the survival of MM cells (19); however, to the best of our knowledge, the link between miR-1343 and ATG7 in the pathogenesis of MM has not yet been investigated. Therefore, the present study explored the mechanism underlying inhibition of MM cell autophagy by miR-1343-3p binding to ATG7 to clarify the regulatory role of miR-1343-3p in MM.

Materials and methods

Cell culture. MM cells (U266 and RPMI-8226) were obtained from China Center for Type Culture Collection (Shanghai, China) and cultured in Eagle's minimum essential medium (Gibco; Thermo Fisher Scientific, Inc.) containing 10% fetal bovine serum (Shanghai ExCell Biology, Inc.) and 1% penicillin-streptomycin (Beyotime Institute of Biotechnology) at 37˚C and 5% CO_2. When the cells reached 80% confluence, they were digested at 37˚C for 2 min with 0.25% trypsin and passaged onto a 6-well plate at a density of $2x10^5$ cells/well.

miR-1343-3p mimic, inhibitor and siRNA transfection. miR-1343-3p mimic, inhibitor and pre-miR-scrambled (Scr) were obtained from Shanghai GenePharma Co., Ltd. (Table I). miRNA mimic and inhibitor were transfected into 293T (China Center for Type Culture Collection), U266 and RPMI-8266 cells using Lipofectamine® 2000 reagent (Invitrogen; Thermo Fisher Scientific, Inc.) according to the manufacturer's protocol. The concentration of nucleic acids used for transfection was 50 nM. The transfection was conducted at room temperature for 20 min for the complex formation, and then cells were incubated at 37˚C in a 5% CO_2 incubator. Following transfection, cells were incubated for 24-48 h before subsequent experimentation. Total RNA was extracted from cells using TRIzol™ (Invitrogen; Thermo Fisher Scientific, Inc.) and reverse-transcribed into cDNA using RT-PCR kit (Takara Bio, Inc.) according to the manufacturer's instructions. qPCR was performed employing a SYBR Green PCR Master Mix (Takara Bio, Inc.) and CFX96 Real-Time PCR Detection System (Bio-Rad Laboratories, Inc.). The relative mRNA levels of miR-1343-3p and ATG7 were evaluated using GAPDH as an internal reference, according to the Livak method. The primers were purchased from Sangon Biotech Company Co., Ltd. (Table II). qPCR was performed using the following thermocycling conditions: Initial denaturation at 95˚C for 10 min, followed by 40 cycles of denaturation at 95˚C for 15 sec, annealing/extension at 60˚C for 60 sec. The relative expression levels of miR-1343-3p and ATG7 were quantified using the 2^-ΔΔCq method (20).

Table I. miR-1343-3p mimic, inhibitor and pre-miR-Scr sequences.

Item	Sequence, 5'→3'
Hsa-miR-1343-3p inhibitor	GCGAGAGUGCGGGCCCCAGGAG
miR-1343-3p mimic	CUCCUGGGGCCCGCACUCUCGC
pre-miR-Scr	CAGUACUUUUGUGUAGUACAA

miR, microRNA; Scr, scrambled.

Dual-luciferase reporter assay. ATG7 3'UTR segment was inserted into the reporter gene vector to construct the Luc-ATG7 3'UTR gene plasmid. $2x10^5$ 293T cells obtained from China Center for Type Culture Collection (Shanghai, China) were seeded in a 24-well plate at 37˚C for 24 h and cultured until the cell density reached 70%. The Scr group was transfected using Lipofectamine 2000 (Thermo Fisher Scientific, Inc.) with Luc-vector plasmid (500 ng/well) and was co-transfected with Luc-ATG7 3'UTR (50 ng/well) and Scr, whereas experimental group was transfected with Luc-vector plasmid (500 ng/well) and co-transfected with Luc-ATG7 3'UTR (50 ng/well) and miR-1343-3p mimic plasmid (500 ng/well; both Shanghai GenePharma Co., Ltd.). The sequences of miR-1343-3p mimic is 5'-CUCCUGGGGCCCGCACUCUCGC-3', the miR-NCs sequence is 5'-CAGUACUUUUGUGUAGUACAA-3'. The cells were incubated at 37˚C in a culture chamber for 48 h. Dual-Lumi™ dual-luciferase reporter gene detection kit (Beyotime Institute of Biotechnology) was used for detection and fluorescence value was recorded using a multifunctional microplate reader (TECAN-Spark; Tecan Group, Ltd.) comparing the Renilla luciferase activity.

Western blot analysis. A total of $5x10^5$ MM cells (U266 and RPMI-8226) were seeded in a 6-well plate, cultured for 24 h at 37˚C and were then transfected with Scr or miR-1343-3p

Table II. Primer sequences.

Primer	Sequence, 5'→3'
miR-1343-3p forward	ctt aga tat ctc ctg ggg ccc g
miR-1343-3p reverse	cag tgc agg gtc cga ggt
miR-1343-3p RT random primer	gac gta tcc agt gca ggg tcc gag gta ttc gca ctg gat acg acg cga ga
ATG7 forward	cag ttt gcc cct ttt agt agt gc
ATG7 reverse	cca gcc gat act cgt tca gc

ATG7, autophagy-related 7; miR, microRNA; RT, reverse transcription.

inhibitor as aforementioned. The cells were incubated at 37˚C in a culture chamber for 48 h, washed once with PBS at 4˚C and removed from the plate using a cell scraper. The cell suspensions were collected in 1.5-ml centrifuge tubes and centrifuged at 300 x g for 5 min at 4˚C. After removing the supernatant, 100 μl of cell lysis buffer (RAPA buffer, Beyotime Institute of Biotechnology) containing protease inhibitor was added to the centrifuge tube. The cells were gently shaken with a pipette and placed on a shaker on ice for 30 min for cell lysis. The samples were centrifuged at 14,000 x g for 10 min at 4˚C, supernatant was transferred to a new centrifuge tube and the protein concentration was measured using a BCA kit (Beyotime Institute of Biotechnology). The proteins were mixed with 6X loading buffer (cat. no. P0015F; Beyotime, Inc.) and boiled at 100˚C for 10 min, after which, 50 μg protein/lane were subjected to separation by 10% SDS-PAGE and transferred onto a PVDF membrane at a constant voltage of 110 V. After blocking the membrane with 5% skimmed milk powder for 2 h at room temperature, the following primary antibodies were added overnight at 4˚C: Anti-GAPDH (cat. no. sc-32233; 1:2,000, Santa Cruz Biotechnology, Inc.), anti-ATG7 (cat. no. 8558; 1:1,000; Cell Signaling Technology, Inc.), anti-p62 (cat. no. 66184-1-Ig; 1:2,000; Proteintech, Inc.) and anti-Beclin-1 (cat. no. 3738; 1:1,000; Cell Signaling Technology, Inc.). After being rinsed with TBS three times (10 min each), the membranes were treated with secondary antibody tagged with horseradish peroxidase (cat. nos. 7074 and 7076, 1:10,000; Cell Signaling Technology, Inc.) for 2 h at room temperature and washed with TBS three times (10 min each time), then visualized with BeyoECL Plus (Beyotime Institute of Biotechnology). Signals were visualized using an enhanced chemiluminescence detection system (Amersham Imager 680 Analysis Software version 2.0; Cytiva) and analyzed using Image J2 (National Institutes of Health). GAPDH was used as the loading control.

Cell viability assay. U266 and RPMI-8226 cells were seeded at 3,000 cells/well in 96-well plates and cultured at 37˚C overnight. Cells were transfected with Scr or miR-1343-3p inhibitor as aforementioned. After 24 h, the cell culture medium was removed and fresh medium without FBS was added for serum starvation. After 48 h of incubation at 37˚C, cell viability was assessed using a Cell Counting Kit-8 (CCK-8) assay (cat. no. C0037; Beyotime Institute of Biotechnology). To each well, 20 μl CCK-8 solution was added and the cells were incubated for 2 h at 37˚C in the dark. Absorbance was measured at 450 nm using a microplate reader (TECAN-Spark; Tecan Group, Ltd.). Viability is expressed relative to the Scr group.

Statistical analysis. Data analysis was performed using GraphPad Prism version 9.0 (GraphPad Software, Inc.; Dotmatics). For comparisons between two groups, two-tailed unpaired Student's t test was employed. A one-way ANOVA followed by Tukey's post hoc test was used for analyses involving multiple groups. $P<0.05$ was considered to indicate a statistically significant difference. Data are presented as the mean ± SEM of three repeats.

TargetScan. The candidate target gene of miR-1343-3p was predicted using TargetScan (targetscan.org/vert_80/).

Results

miR-1343-3p regulates ATG7 by targeting its 3'UTR. The prediction of miR-1343-3p targets showed ATG7 as a candidate gene. There were five sequence-specific interactions between miR-1343-3p and ATG7 (Fig. 1A). The present study investigated whether miR-1343-3p regulates ATG7 through its 3'UTR by cloning ATG7 3'UTR into a luciferase vector. si-mir exhibited a decrease in luciferase activity with Luc-ATG7 3'UTR but not with NC, which indicated that miR-1343-3p targeted ATG7 through its 3'UTR (Fig. 1B).

miR-1343-3p regulates ATG7 expression in MM cell lines. To confirm the role of miR-1343-3p in regulation of ATG7, the present study detected the mRNA and protein levels of ATG7 in the U266 human MM cell line and in RPMI-8226 human MM peripheral blood B lymphocytes post-transfection. Following miR-1343-3p mimic transfection in U266 and RPMI-8226 cells, miR-1343-3p was successfully overexpressed (Fig. 2A). ATG7 mRNA levels were downregulated in U266 and RPMI-8226 cells post-transfection with miR-1343-3p mimic. Similarly, western blot analysis showed that ATG7 protein levels were downregulated in U266 and RPMI-8226 cells following miR-1343-3p mimic transfection.

By contrast, miR-1343-3p inhibitor transfection significantly downregulated the mRNA levels of miR-1343-3p (Fig. 2B). Furthermore, RT-qPCR and western blot analysis confirmed that ATG7 protein levels were increased following knockdown of miR-1343-3p (Fig. 2B).

A

Position	Predicted consequential pairing of ATG7 (top) and hsa-miR-1343-3p (bottom)	K_D
142-148 of ATG7 3′ UTR	5′ ...UUCCCCCCUCUGCUG----CCCAGGAG...	−3.580
hsa-miR-1343-3p	3′ CGCUCUCACGCCCGGGGUCCUC	
293-299 of ATG7 3′ UTR	5′ ...GACUGAUAGCCAUCCCCCAGGAU...	−3.176
hsa-miR-1343-3p	3′ GAUGUCUCCUCUUCGGGUCCUU	
908-914 of ATG7 3′ UTR	5′ ...GCUGUGAGGCCCCAACCCAGGAG....	−3.621
hsa-miR-1343-3p	3′ GAUGUCUCCUCUUC--GGGUCCUU	
1311-1317 of ATG7 3′ UTR	5′ ...UUUUUUUUUCUUCUUCCAGGAAA...	−3.60
hsa-miR-1343-3p	3′ CGCUCUCACGCCCGGGGUCCUC	
1601-1607 of ATG7 3′ UTR	5′ ...GACAAAGAGACCUGUCCCAGGAG...	−3.491
hsa-miR-1343-3p	3′ GAUGUCUCCUCUUCGGGUCCUU	

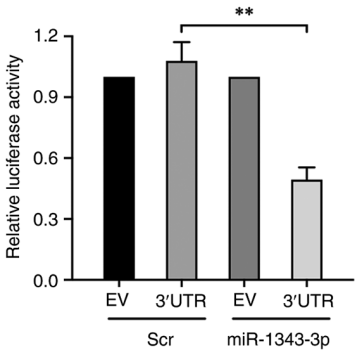

Figure 1. Interaction between miR-1343-3p and ATG7 3'UTR. (A) Sequence alignment and predicted binding sites between miR-1343-3p and ATG7 3'UTR. (B) Cells were transfected with EV or a vector containing the ATG7 3'UTR in the presence or absence of miR-1343-3p mimic for 48 h and the luciferase activity was subsequently measured. **P<0.01. ATG7, autophagy-related 7; 3'UTR, 3' untranslated region; miR, microRNA; EV, empty vector; Scr, scrambled.

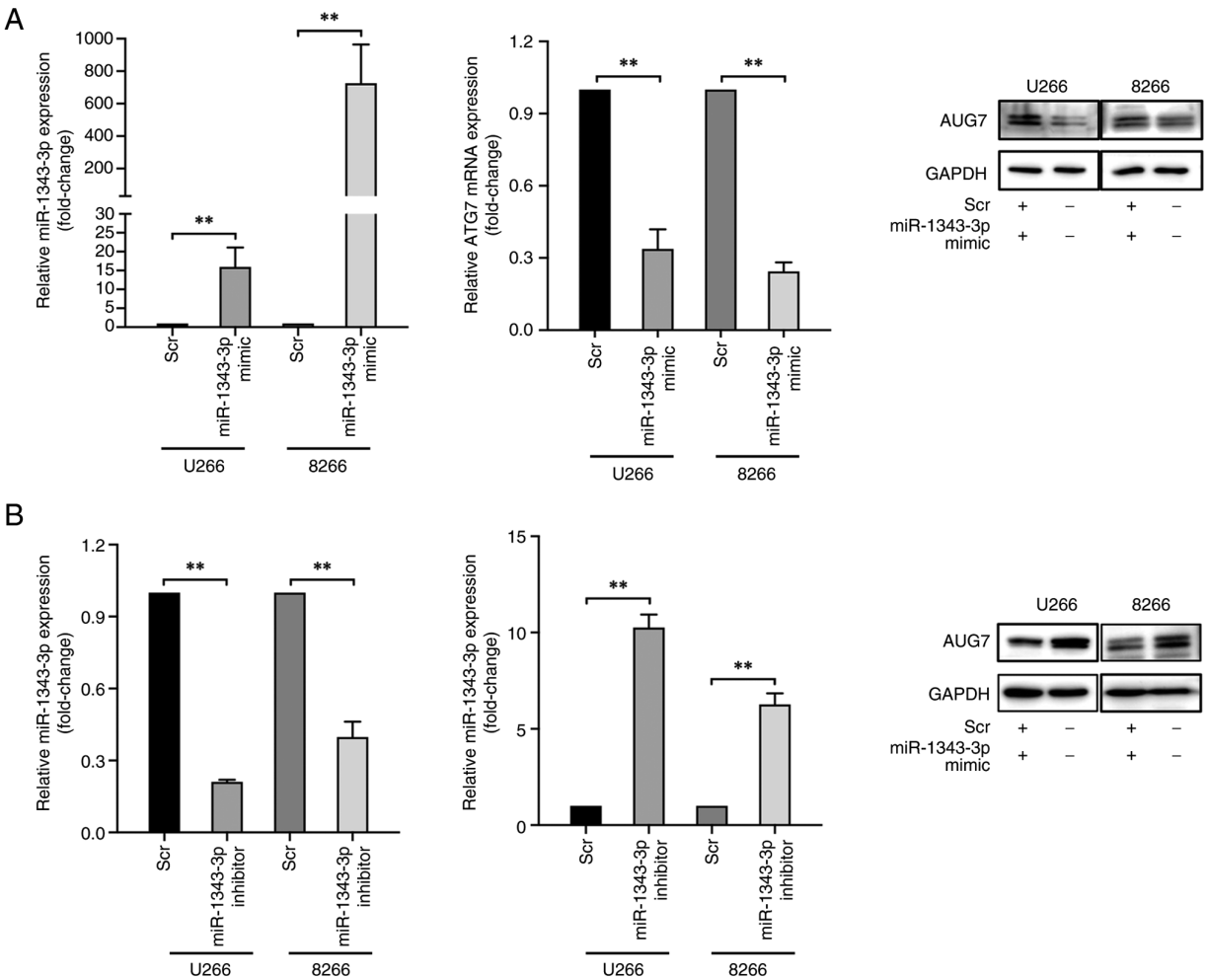

Figure 2. miR-1343-3p regulates ATG7 in multiple myeloma cells. Reverse transcription-quantitative PCR analysis of miR-1343-3p and ATG7 mRNA levels and western blotting of ATG7 protein levels in U266 and RPMI-8226 cells transfected either with miR-1343-3p (A) mimic, (B) inhibitor or miR-16. **P<0.01 vs. Scr. ATG7, autophagy-related 7; miR, microRNA; Scr, scrambled.

miR-1343-3p is involved in MM cell autophagy. As the ATG7 gene encodes an E1-like activating enzyme that is key for autophagy and cytoplasmic-to-vacuole transport and miR-1343-3p regulated ATG7, the present study investigated the role of miR-1343-3p in MM cell autophagy. Protein expression of p62 was significantly decreased and relative expression

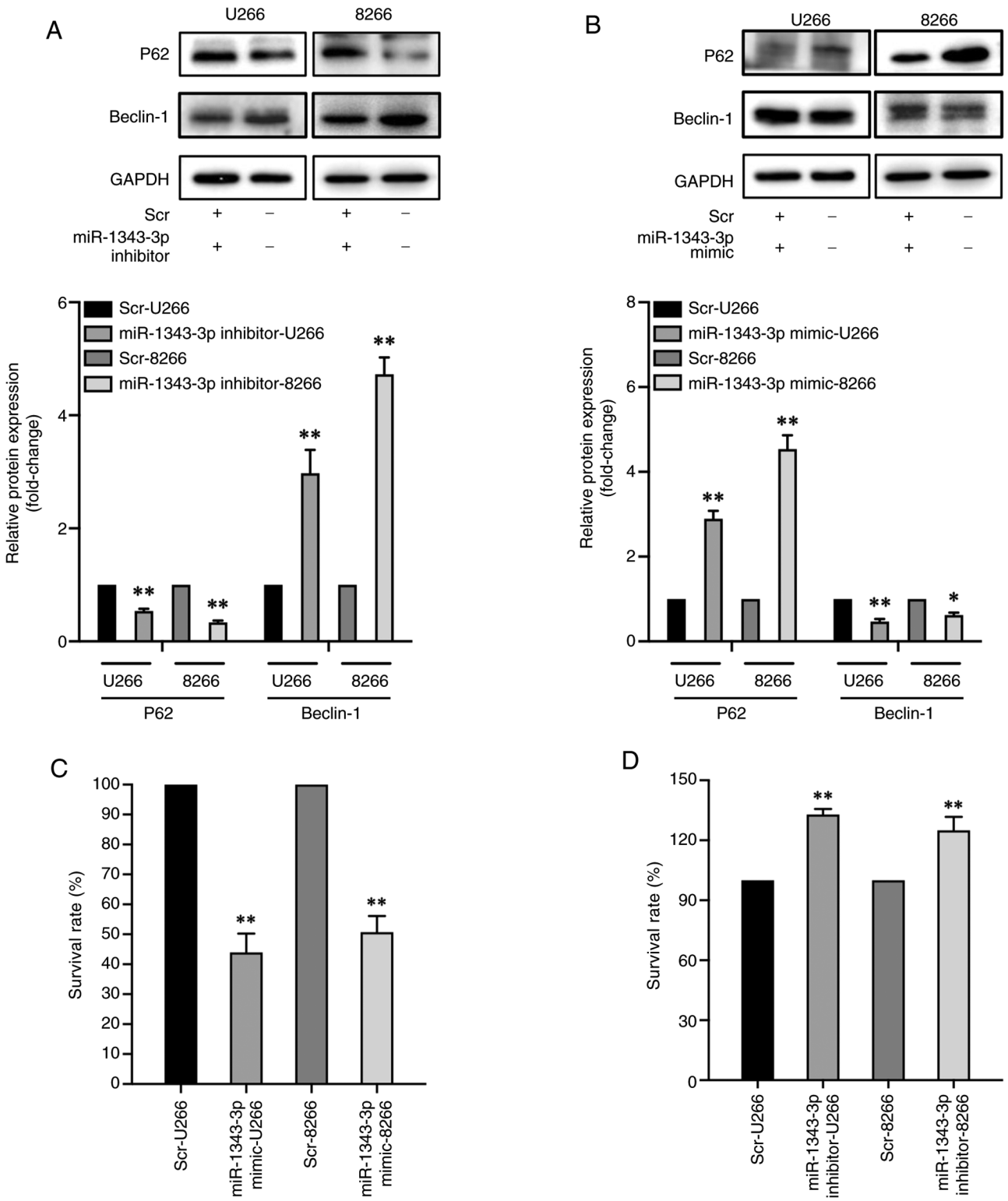

Figure 3. miR-1343-3p regulates autophagy in multiple myeloma cells. Autophagy-associated protein levels in U266 and RPMI-8226 cells transfected with miR-1343-3p (A) inhibitor and (B) mimic or miR-16 oligonucleotides. Viability of U266 and RPMI-8226 cells transfected with miR-1343-3p (C) inhibitor and (D) mimic or miR-16 oligonucleotides. **P<0.01, *P<0.05 vs. Scr group. miR, microRNA; Scr, scrambled.

of Beclin-1 was significantly elevated in MM cells transfected with the miR-1343-3p inhibitor (Fig. 3A). However, protein expression of p62 was significantly elevated and the expression of Beclin-1 was significantly decreased in cells transfected with the miR-1343-3p mimic (Fig. 3B). These data indicated that miR-1343-3p suppressed onset of autophagy in MM cells.

Subsequently, cell viability following miR-1343-3p upregulation or downregulation was detected using CCK-8 assay. miR-1343-3p inhibition increased U266 and RPMI-8226 cell survival rate by ~30%, whereas miR-1343-3p overexpression decreased the U266 and RPMI-8226 cell survival rate by ~50% when cells were serum-starved for 48 h (Fig. 3C and D).

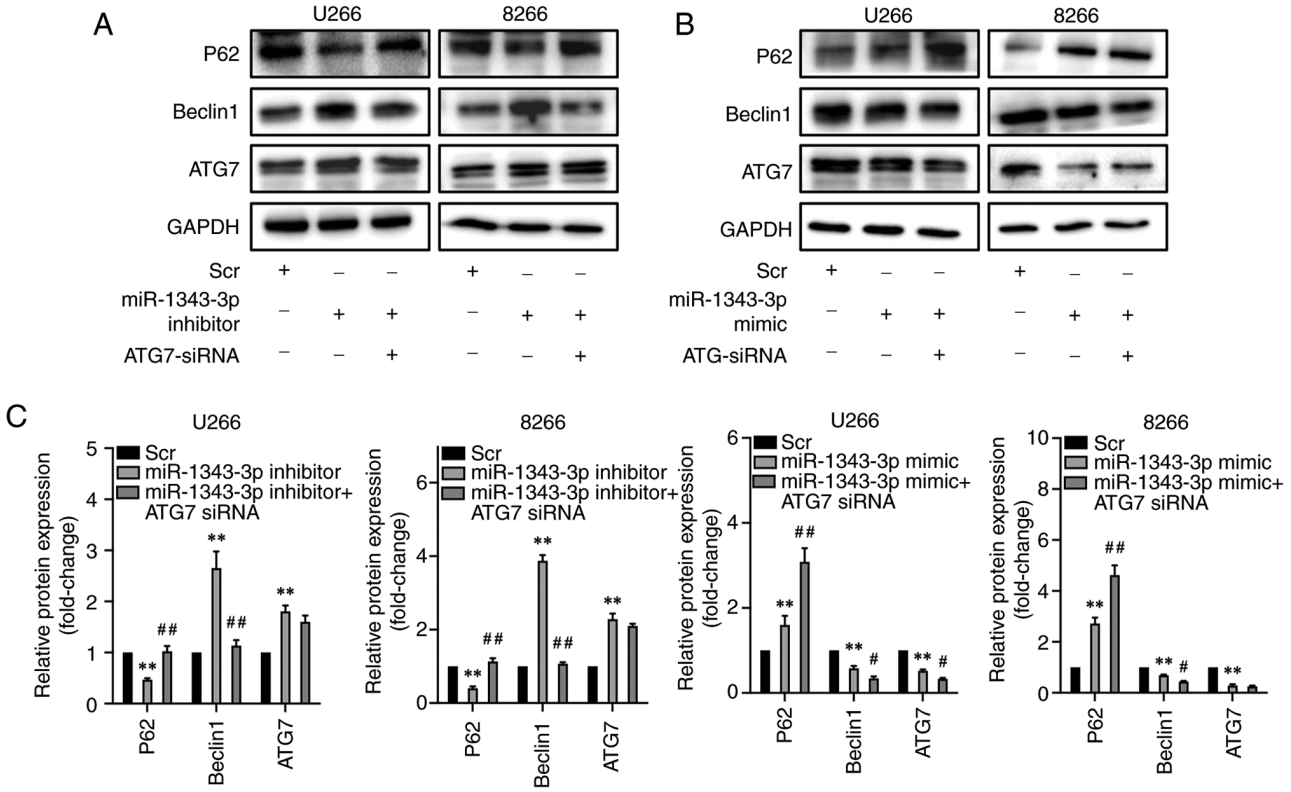

Figure 4. Verification of regulatory effects of miR-1343-3p on ATG7 and autophagy in MM cells. Western blot analysis of ATG7, p62 and Beclin1 protein levels in MM cells transfected with miR-1343-3p (A) inhibitor and (B) mimic with or without ATG7 knockdown. **P<0.01 compared with Scr group; $^{\#\#}$P<0.01, $^{\#}$P<0.05 compared with miR-1343-3p inhibitor group. ATG7, autophagy-related 7; miR, microRNA; MM, multiple myeloma; si, small interfering; Scr, scrambled.

Verification of the regulatory effect of miR-1343-3p on ATG7 and autophagy in MM cell. miR-1343-3p inhibitor elevated Beclin1 expression and decreased the relative expression of p62 (Fig. 4A). However, co-transfecting cells with ATG7 siRNA and the miR-1343-3p inhibitor reversed these phenomena; Beclin1 protein expression was decreased and p62 protein levels increased compared with in the cells transfected with miR-1343-3p inhibitor alone.

By contrast, ATG7 siRNA transfection further decreased ATG7 and Beclin1 expression and further increased p62 levels (Fig. 4B), which suggested that ATG7 may be a downstream gene of miR-1343-3p and miR-1343-3p inhibited autophagy by targeting ATG7.

Discussion

The present study used TargetScan to predict whether ATG7 was a candidate target gene of miR-1343-3p and confirmed the interaction between miR-1343-3p and the ATG7 3'UTR using a dual-luciferase reporter assay. In MM U266 and RPMI-8226 cells, miR-1343-3p mimic transfection decreased ATG7 mRNA and protein levels, whereas miR-1343-3p inhibition increased ATG7 expression. In addition, miR-1343-3p inhibition promoted U266 and RPMI-8226 cell survival by inducing autophagy via ATG7. Conversely, miR-1343-3p mimic transfection inhibited U266 and RPMI-8226 cell survival.

miR-1343-3p downregulation serves an important role in multiple types of cancer, including lung (21), colon and prostate cancer (22). Activating Transcription Factor 2) -induced GAS8-AS1 expression has been shown to promote autophagy by regulating the GAS8-AS1/miR-1343-3p/ATG7 pathway, consistent with *in vivo* results; enhancing expression of these molecular pathways may alter the occurrence and development of malignant cells (15). In the present study, miR-1343-3p was predicted to target ATG7. The luciferase assay indicated that miR-1343-3p bound ATG7 3'UTR and decreased its luciferase activity. Meanwhile, expression levels of ATG7 were revealed to be downregulated in MM cell lines transfected with a miR-1343-3p mimic. These results indicated that miR-1343-3p could bind directly to ATG7 and downregulate its expression in MM cells.

MM is a genetically complex and heterogeneous malignancy with a 5-year survival rate of ~60% (23); MM is currently regarded as an incurable disease (24). Its pathological mechanism is associated with unchecked proliferation and accumulation of antibody-secreting plasma cells (25), most of which are concentrated in the bone marrow. This accumulation leads to elevated levels of immunoglobulins in the serum and an overproduction of their light chains, which can contribute to organ damage and complications such as kidney dysfunction in multiple myeloma patients (26). MM is a complex disease involving poor prognosis, genomic instability, aberrant cytokines and a complex microenvironment that contribute to the development and progression of the disease (27). The incidence of MM increased between 1999 and 2020, with a 40% rise in the United States and a ~130% increase globally since 1990 (28,29). With the application of new drugs in combination with hematopoietic stem cell transplantation, the

treatment outcome and prognosis of patients with MM has notably improved (30). However, the pathological mechanism of MM is still unknown.

miR-449, miR-181a and miR-181b are highly expressed in the blood of patients with MM and miR-21, miR-106b-25 cluster and miR-181a/b may serve oncogenic roles in the malignant transformation of MM and monoclonal Gammopathy of Undetermined Significance (31). Additionally, a number of miRNAs have been reported to be associated with prognosis of MM. Patients with high expression of oncogenic miRNAs, such as miR-17-92 and miR-194, have shorter progression-free survival (PFS); patients with low expression of tumor-suppressing miRNAs, such as miR-15 and miR-410, also have a shorter PFS (32). Furthermore, downregulation of miRNAs in MM cell lines or patients suggests that increasing their expression might reduce the proliferation of MM cells *in vitro*, whereas decreasing their expression might enhance the proliferation of these cells, which including miR-34a, miR-137/197, miR-1271 and miR-125b (33-36). Effective nanoparticles, liposomes or viral vectors can be designed to deliver miRNAs or anti-miRNAs to tumor cells. Combining miRNA therapy with traditional chemotherapy, targeted therapy or immunotherapy may enhance therapeutic effects. For example, combination of miR-29b with bortezomib has been shown to exert synergistic antitumor effects (37). However, no miRNA is currently considered a definitive diagnostic or prognostic marker for MM in clinical practice, nor has any been used in clinical trials for patients with MM. Therefore, researching the therapeutic potential and anticancer mechanisms of miRNAs in MM is key.

Autophagy is a physiological process that involves cells destroying and recycling their own non-essential or damaged parts (28). It is primarily controlled by the ATG gene family and signaling pathways, including the mTOR and AMPK signaling pathway, liver Kinase B1), ULK1 (Unc-51-Like Kinase 1) and Beclin1 (29). In cancer cells, autophagy encourages apoptosis and prevents the growth of tumors; however, recent research has demonstrated that stressors, such as hypoxia and nutrient deprivation, are present in the environment where cancer cells grow and that under these stressors, cancer cells obtain energy and nutrients through autophagy, which promotes cancer cell proliferation and apoptotic resistance (23). Numerous studies have demonstrated that autophagy is key for the proliferation of plasma cells, as well as the pathophysiology of MM (19). MM cells produce large amounts of monoclonal immunoglobulins that induce endoplasmic reticulum stress and autophagy can degrade excess protein aggregates, thereby protecting MM cells (38). Therefore, autophagy serves an irreplaceable role in the survival of MM cells (11). The current study showed that miR-1343-3p inhibition promoted U266 and RPMI-8226 cell survival by inducing autophagy via ATG7. Conversely, miR-1343-3p mimic transfection inhibited U266 and RPMI-8226 cell survival. The present results revealed a novel mechanism of MM progression mediated by miR-1343-3p.

In conclusion, the present findings indicated that miR-1343-3p can bind to ATG7 3'UTR and overexpression of miR-1343-3p may decrease ATG7 expression levels and inhibit MM cell survival. To the best of our knowledge, no direct data show the roles of miR-1343-3p in development of MM; however, miR-1343-3p and ATG7 may serve as novel biomarkers or therapeutic targets for MM.

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Availability of data and materials

The data generated in the present study may be requested from the corresponding author.

Authors' contributions

LY and SC conceived the study, designed and performed experiments, analyzed data and wrote the manuscript. JC conceived the study. YG, XD, CD and WW performed the experiments. YG and GC designed the methodology. GC performed experiments and reviewed the manuscript. YG and LY confirm the authenticity of all the raw data. All authors have read and approved the final manuscript.

Ethics approval and consent to participate

Not applicable.

Patient consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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